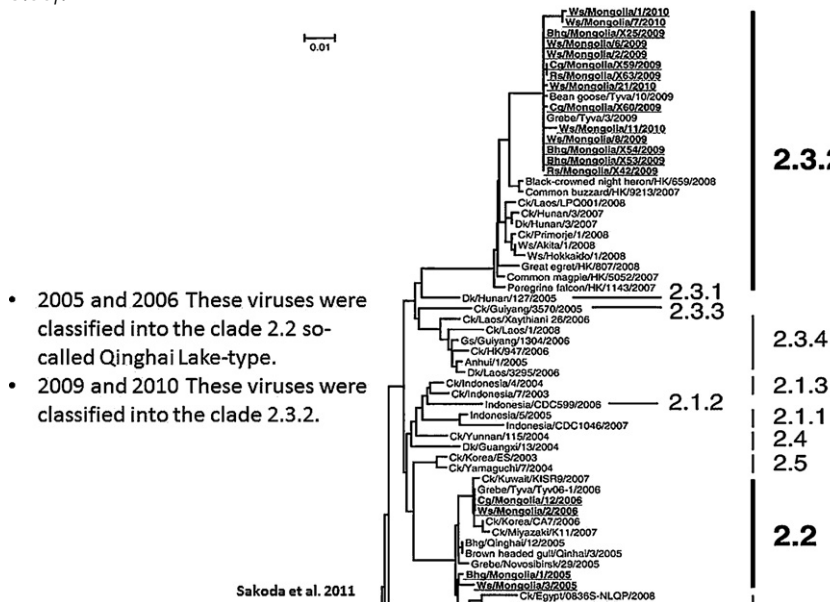


were isolated from a whooper swan and a common goldeneye in May 2006 in Khunt and Erkhel Lakes. These viruses were classified into the clade 2.2 so-called Qinghai Lake-type.

In May 2009, H5N1 viruses were isolated from 3 whooper swans in Doityn Tsagaan Lake. In late July 2009, H5N1 viruses were also isolated from dead wild birds, 3 bar-headed geese, 2 ruddy shel ducks, and 2 common goldeneyes in Doroo Lake. In May 2010, H5N1 viruses were isolated from 4 whooper swans in Ganga Lake. These viruses were classified into the clade 2.3.2. The IVPI was high/2.97–3.00/.



Phylogenetic trees of the HA genes of H5 influenza viruses

Conclusion: The phylogenetic differences of the H5N1 isolates from 2005, 2006, and 2009, 2010 indicate that the role of the migratory birds in Mongolia in the AIV mutation should be clarified. So, main strategy of to combat and prevent from the HPAI is continuous active-surveillance and early clarification for mutation of AIV in wild birds.

Therefore, it is necessary to continue the research on avian influenza in Mongolia.

<http://dx.doi.org/10.1016/j.ijid.2012.05.643>

Type: Poster Presentation

Final Abstract Number: 57.009

Session: Zoonoses & Infections in Animals

Date: Saturday, June 16, 2012

Time: 12:45–14:15

Room: Poster & Exhibition Area

Serological evidence of Hepatitis E Virus in pigs in Bangladesh

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Background: Hepatitis E Virus (HEV) is the most common cause of viral hepatitis globally. Pigs may act as a reservoir of HEV and antibodies to HEV have been found in pigs in neighboring coun-

tries including India and Nepal. In Bangladesh, studies suggest that 30–60% of acute human viral hepatitis is due to HEV. To understand the pig's role as a reservoir for HEV in Bangladesh, we conducted a serological survey to identify evidence of HEV infection among pig populations.

Methods: We collected blood samples from 100 pigs from three slaughterhouses in Gazipur district between January–June 2011. We interviewed the slaughterhouse owners and/or pig herder to record data on herd size, age, sex and breed of pigs. We tested the

sera for HEV-specific IgG, IgM and IgA antibody through competitive enzyme-linked immunosorbent assay.

Results: Out of 100 swine sera, 82% (n = 82) had detectable antibody against HEV [95% confidence interval (CI): 74.3–89.6]. These pigs were raised in herds in six districts of Bangladesh and the numbers of pigs having HEV antibody varied among the districts: Gazipur (93%, n = 13); Barisal (88%, n = 29); Jessore (84%, n = 21); Rajshahi (82%, n = 9); Mymensingh (60%, n = 3) and Pabna (58%, n = 7). Compared to the pigs that lacked HEV antibody, pigs with HEV antibody were older [21.5 months vs. 9.6 months, p < 0.001], were more likely to be raised in larger herds (mean herd size: 194 pigs vs. 125 pigs, p = 0.008), were more frequently male (60%, vs. 22% p = 0.004), and were more frequently indigenous breed (89% vs. 39%, p < 0.001).

Conclusion: This study provides evidence that the virus causing HEV disease in pigs is circulating in Bangladesh. We recommend identifying the genotypes of HEV in pigs to determine their role as a possible reservoir for zoonotic transmission to humans in Bangladesh.

<http://dx.doi.org/10.1016/j.ijid.2012.05.644>